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- (viii) ATTORNEY/AGENT INFORMATION:
 (A) NAME: Muetting, Ann M.
 (B) REGISTRATION NUMBER: 33,977
 (C) REFERENCE/DOCKET NUMBER: 110.00230101
- (ix) TELECOMMUNICATION INFORMATION:
 (A) TELEPHONE: 612-305-1217
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(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1858 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

CTCGGGTAAC TTCTTGAGCG CGGCCACAGC AGCCTTGATC ATGAAGGCGA GCATGGTGAC	60
CTTGACGCCG CTCTTTTCGT TCTCTTTGTT GAACTGCACG CGAAAGGCTT CCAGGTCGGT	120
GATGTCCGCG TCGTCGTGGT TGGTGACGTG CGGGATGACC ACCCAGTTGC GGTGCAGGTT	180
TTTCGATGGC ATAATATCTG CGTTGCGACG TGTAACACAC TATTGGAGAC ATATCATGCA	240
AACGCTCAGC ATCCAGCACG GTACCCTCGT CACGATGGAT CAGTACCGCA GAGTCCTTGG	300
GGATAGCTGG GTTCACGTGC AGGATGGACG GATCGTCGCG CTCGGAGTGC ACGCCGAGTC	360
GGTGCCCTCCG CCAGCGGATC GGGTGATCGA TGCACGCGGC AAGGTCGTGT TACCCGGTTT	420
CATCAATGCC CACACCCATG TGAACCAGAT CCTCCTGCGC GGAGGGCCCT CGCACGGACG	480
TCAATTCTAT GACTGGCTGT TCAACGTTGT GTATCCGGGA CAAAAGGCGA TGAGACCGGA	540
GGACGTAGCG GTGGCGGTGA GGTGTATTG TGCGGAAGCT GTGCGCAGCG GGATTACGAC	600
GATCAACGAA AACGCCGATT CGGCCATCTA CCCAGGCAAC ATCGAGGCCG CGATGGCGGT	660
CTATGGTGAG GTGGGTGTGA GGGTCGTCTA CGCCCGCATG TTCTTTGATC GGATGGACGG	720
GCGCATTCAA GGGTATGTGG ACGCCTTGAA GGCTCGCTCT CCCCAGTCG AACTGTGCTC	780
GATCATGGAG GAAACGGCTG TGGCCAAAGA TCGGATCACA GCCCTGTCAG ATCAGTATCA	840
TGGCACGGCA GGAGGTCGTA TATCAGTTTG GCCCCTCCT GCCACTACCA CGGCGGTGAC	900
AGTTGAAGGA ATGCGATGGG CACAAGCCTT CGCCCGTGAT CGGGCGGTAA TGTGGACGCT	960
TCACATGGCG GAGAGCGATC ATGATGAGCG GATTCATGGG ATGAGTCCCG CCGAGTACAT	1020
GGAGTGTTAC GGA CTCTTGG ATGAGCGTCT GCAGGTCGCG CATTGCGTGT ACTTTGACCG	1080
GAAGGATGTT CGGCTGCTGC ACCGCCACAA TGTGAAGGTC GCGTCGCAGG TTGTGAGCAA	1140
TGCCTACCTC GGCTCAGGGG TGGCCCCCGT GCCAGAGATG GTGGAGCGCG GCATGGCCGT	1200

GGGCATTGGA ACAGATAACG GGAATAGTAA TGA TCCGCA AACATGATCG GAGACATGAA 1260
 GTTTATGGCC CATATTCACC GCGCGGTGCA TCGGGATGCG GACGTGCTGA CCCCAGAGAA 1320
 GATTCTTGAA ATGGCGACGA TCGATGGGGC GCGTTCGTTG GGAATGGACC ACGAGATTGG 1380
 TTCCATCGAA ACCGGCAAGC GCGCGGACCT TATCCTGCTT GACCTGCGTC ACCTCAGACG 1440
 ACTCTCACAT CATTTGGCGG CCACGATCGT GTTTCAGGCT TACGGCAATG AGGTGGACAC 1500
 TGTCTTGATT GACGGAAACG TTGTGATGGA GAACCGCCGC TTGAGCTTTC TTCCCCCTGA 1560
 ACGTGAGTTG GCGTTCCTTG AGGAAGCGCA GAGCCGCGCC ACAGCTATTT TGCAGCGGGC 1620
 GAACATGGTG GCTAACCCAG CTTGGCGCAG CCTCTAGGAA ATGACGCCGT TGCTGCATCC 1680
 GCCGCCCCCTT GAGGAAATCG CTGCCATCTT GCGCGGCTC GGATTGGGGG GCGGACATGA 1740
 CCTTGATGGA TACAGAATTG CCATGAATGC GGCATTCCG TCCTTCGCTC GTGTGGAATC 1800
 GTTGGTAGGT GAGGGTCGAC TCGGGCGCC AGCTTCCCGA AGAGGTGAAA GGCCCGAG 1858

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 473 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met	Gln	Thr	Leu	Ser	Ile	Gln	His	Gly	Thr	Leu	Val	Thr	Met	Asp	Gln
1				5				10					15		
Tyr	Arg	Arg	Val	Leu	Gly	Asp	Ser	Trp	Val	His	Val	Gln	Asp	Gly	Arg
			20				25					30			
Ile	Val	Ala	Leu	Gly	Val	His	Ala	Glu	Ser	Val	Pro	Pro	Pro	Ala	Asp
		35				40					45				
Arg	Val	Ile	Asp	Ala	Arg	Gly	Lys	Val	Val	Leu	Pro	Gly	Phe	Ile	Asn
	50				55					60					
Ala	His	Thr	His	Val	Asn	Gln	Ile	Leu	Leu	Arg	Gly	Gly	Pro	Ser	His
65				70				75					80		

Gly Arg Gln Phe Tyr Asp Trp Leu Phe Asn Val Val Tyr Pro Gly Gln
 85 90 95

Lys Ala Met Arg Pro Glu Asp Val Ala Val Ala Val Arg Leu Tyr Cys
 100 105 110

Ala Glu Ala Val Arg Ser Gly Ile Thr Thr Ile Asn Glu Asn Ala Asp
 115 120 125

Ser Ala Ile Tyr Pro Gly Asn Ile Glu Ala Ala Met Ala Val Tyr Gly
 130 135 140

Glu Val Gly Val Arg Val Val Tyr Ala Arg Met Phe Phe Asp Arg Met
 145 150 155 160

Asp Gly Arg Ile Gln Gly Tyr Val Asp Ala Leu Lys Ala Arg Ser Pro
 165 170 175

Gln Val Glu Leu Cys Ser Ile Met Glu Glu Thr Ala Val Ala Lys Asp
 180 185 190

Arg Ile Thr Ala Leu Ser Asp Gln Tyr His Gly Thr Ala Gly Gly Arg
 195 200 205

Ile Ser Val Trp Pro Ala Pro Ala Thr Thr Thr Ala Val Thr Val Glu
 210 215 220

Gly Met Arg Trp Ala Gln Ala Phe Ala Arg Asp Arg Ala Val Met Trp
 225 230 235 240

Thr Leu His Met Ala Glu Ser Asp His Asp Glu Arg Ile His Gly Met
 245 250 255

Ser Pro Ala Glu Tyr Met Glu Cys Tyr Gly Leu Leu Asp Glu Arg Leu
 260 265 270

Gln Val Ala His Cys Val Tyr Phe Asp Arg Lys Asp Val Arg Leu Leu
 275 280 285

His Arg His Asn Val Lys Val Ala Ser Gln Val Val Ser Asn Ala Tyr
 290 295 300

Leu Gly Ser Gly Val Ala Pro Val Pro Glu Met Val Glu Arg Gly Met
 305 310 315 320

Ala Val Gly Ile Gly Thr Asp Asn Gly Asn Ser Asn Asp Ser Ala Asn
 325 330 335

Met Ile Gly Asp Met Lys Phe Met Ala His Ile His Arg Ala Val His
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